Reviewer 2 v.1

Comments to the Author

I thank the authors for this clear and informative manuscript. In this retrospective observational cohort study Melamed et al. compared two groups of patients: a group with influenza infection (including more than 50% of H1N1) and a group with other viral infections. This manscript aimed to describe secondary pulmonary infections and outcome of these patients in Non-Influenza Viral Respiratory Infection. They observed that co-infections with bacteria are also frequent in this context.

Major comment:

- Inclusion criteria: “positive results from viral studies within the first 10 days of admission”; exclusion criteria: “Patients with onset of secondary pneumonia late into the admission (defined as more than two weeks) were excluded”. If I understand correctly: patients were included if they had bacterial co-infection at admission and up to 15 days post admission. There is a mix of community acquired pneumonia (i.e. bacterial infection acquired before/during/after viral infection outside the hospital) and health associated pneumonia (nosocomial pneumonia). These two diseases are strictly distinct regarding physiopathology, pathogens, etc…It is not possible to perform a global analyze. It is a critical point.

- There is an important difference between the two groups regarding the number of lung-transplant and immunocompromised patients (higher in the NI group). The immunocompromised status is known to favor bacterial or fungal infections and may bias the final significant difference of secondary pneumonia in the NI group (44%) compared to the VI group (23%). Furthermore, the presence of CMV or HSV pulmonary infections may sign a severe immunosuppression in some patients of the study increasing the bias between the 2 groups. Finally, these immunocompromised patients are more likely to be infected by specific types of microorganisms because of their more frequent contact with the healthcare system. It seems complicate to extrapolate these results to the general population.

- The screening Methology used ICD-9 codes. While this method is known acknowledged as a powerful epidemiologic tool, the codes for microbial etiology have poor performance (especially ten years ago) and it is not clear how it is used here. Were the 2824 admission files reviewed or screened by ICD-9 codes? Can you: (i) clarify this point and (ii) refer to articles that validate this strategy.

Minor comments:

- The correct nomenclature for the influenza virus responsible for the 2009 pandemic is A(H1N1)pdm09. Please edit accordingly.

- The paper deserves to be clearer about the ICU stay of patients and ideally proportion of mechanically ventilated patients. The number of patients admitted to ICU is described in the figure 3, but must be also indicated in the text or even in the table 2, ideally with a score to compare the patients' gravity. The proportion of ICU patients seems higher in the NI group.

- The paper deserves to be also clearer about the "respiratory symptoms" having justified a hospitalization and if possible, objective vital parameters such as respiratory rate. Criteria based on scores validated in pulmonary infections would bring even more informations (e.g. CRB65, CURB65).

- In the VI group, it would be preferable if the authors provide more details about the proportion of secondary infected patients specifically in the A(H1N1)pdm09-infected patients.

- H1N1 pandemic in 2009 was a specific time in the hospitals. In the VI group, the study mixes H1N1 patients (> 50%) and with "most classic" influenza infection. Can we so easily mix these categories of patients?

- The predominance of the S. aureus as the first found pathogen in the VI group is, as you say in your paper, quite astonishing and very interesting. In ICU, the study by Yap et al. have found an increase in Methicillin-Resistant Staphylococcus aureus (MRSA) implicated in ventilator-acquired pneumonia (VAP) after the SARS-CoV1 pandemic in 2002-2003. It is important to note that approximately half of the VI group was infected by H1N1, also during an epidemic time: the secondary S. aureus infections in your study may have been caused by MRSA which may emerge in epidemic situations, because of non-scrupulous hygiene precautions (e.g. increased use of gloves, less frequent hand hygiene) or heavy use of antimicrobials active against gram-negative organisms. What was the proportion of MRSA infections? The high proportion of S. aureus infections can be eventually explained by a bacterial cross-transmission because of the epidemic situation, and we probably need a clarification about this eventuality.